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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/528,611	03/21/2005	Steven Gutteridge	BB1533USPCT	7575

7590 05/15/2007

E I du Pont de Nemours & Company
Legal Patents
Wilmington, DE 19898

EXAMINER	
LI, RUIXIANG	

ART UNIT	PAPER NUMBER
1646	

MAIL DATE	DELIVERY MODE
05/15/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/528,611	GUTTERIDGE ET AL.	
	Examiner	Art Unit	
	Ruixiang Li	1646	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 1 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-33* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) _____ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *1-33* are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *Sequence alignment*.

Election/Restrictions

1. Restriction is required under 35 U.S.C. 121 and 372.

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In accordance with 37 CFR 1.499, applicant is required, in response to this action, to elect a single invention to which the claims must be restricted.

I. Claims 1-9, drawn to an isolated nucleotide fragment encoding a ryanodine receptor, a vector, and a host cell.

II. Claim 10, drawn to a method to isolate nucleic acid fragments encoding ryanodine receptors and related polypeptides.

III. Claims 11-15, drawn to an isolated polypeptide having ryanodine receptor activity.

IV. Claims 16-20, drawn to a method for evaluating at least one compound for its ability to modulate calcium homeostasis or a method for evaluating at least compound which modulates ryanodine receptor activity.

V. Claims 21 and 24-33, drawn to an isolated nucleic acid fragment encoding an insect ion channel, a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel, and a recombinant constructor.

VI. Claims 22 and 23, drawn to a method for identifying a nucleic acid sequence encoding an insect ion channel.

2. The inventions listed as Groups I-VI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The technical feature linking Groups I-VI appears to be an isolated nucleotide fragment encoding a ryanodine receptor. However, claims 1-5 and 7-9 are anticipated by Takeshima et al. (FEBS Letters 337:81-87, 1994). Takeshima et al. teach a ryanodine receptor (Fig. 2) and its encoding DNA sequence (page 82). Since the ryanodine receptor of Takeshima et al. shares a high degree of homology with the amino acid sequence of SEQ ID NO: 128 of the present invention (see attached sequence alignment), the complementary sequence of the DNA sequence of Takeshima et al. comprises the complement of (a) of claim 1. It is noted that claim 1, part (b), does not require the complement of (a) is a full complement of (a) of claim 1 (i.e., over its entire length). Takeshima et al. further teach a recombinant construct and a host cell comprising the DNA sequence (bottom of right column of page 81) and use of CHO cells as host cells (top of right column of page 81). Thus, the teachings of Takeshima et al. meet the limitations of claims 1-5 and 7-9.

Therefore, the technical feature linking the inventions of Groups I-VI does not constitute a special technical feature as defined by PCT Rule 13.2, as it does not define a contribution over the prior art.

3. The special technical features of Groups I-III are an isolated nucleotide fragment encoding a ryanodine receptor, a vector, and a host cell, a method to isolate nucleic acid fragments encoding ryanodine receptors and related polypeptides, and an

2. The inventions listed as Groups I-VI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The technical feature linking Groups I-VI appears to be an isolated nucleotide fragment encoding a ryanodine receptor. However, claims 1-5 and 7-9 are anticipated by Takeshima et al. (FEBS Letters 337:81-87, 1994). Takeshima et al. teach a ryanodine receptor (Fig. 2) and its encoding DNA sequence (page 82). Since the ryanodine receptor of Takeshima et al. shares a high degree of homology with the amino acid sequence of SEQ ID NO: 128 of the present invention (see attached sequence alignment), the complementary sequence of the DNA sequence of Takeshima et al. comprises the complement of (a) of claim 1. It is noted that claim 1, part (b), does not require the complement of (a) is a full complement of (a) of claim 1 (i.e., over its entire length). Takeshima et al. further teach a recombinant construct and a host cell comprising the DNA sequence (bottom of right column of page 81) and use of CHO cells as host cells (top of right column of page 81). Thus, the teachings of Takeshima et al. meet the limitations of claims 1-5 and 7-9.

Therefore, the technical feature linking the inventions of Groups I-VI does not constitute a special technical feature as defined by PCT Rule 13.2, as it does not define a contribution over the prior art.

3. The special technical features of Groups I-III are an isolated nucleotide fragment encoding a ryanodine receptor, a vector, and a host cell; a method to isolate nucleic acid fragments encoding ryanodine receptors and related polypeptides; and an

isolated polypeptide having ryanodine receptor activity, respectively. The special technical features of Groups IV-VI are a method for evaluating at least one compound for its ability to modulate calcium homeostasis or a method for evaluating at least compound which modulates ryanodine receptor activity; an isolated nucleic acid fragment encoding an insect ion channel, a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel, and a recombinant constructor; and a method for identifying a nucleic acid sequence encoding an insect ion channel, respectively.

4. Accordingly, Groups I-VI are not so linked by the same or a corresponding special technical feature as to form a single general inventive concept. Thus, unity of invention is lacking and restriction is appropriate.

5. Furthermore, this application contains claims directed to the following amino acid/nucleic acid sequences and each amino acid/nucleic acid sequence represents an *additional* invention group:

(i). amino acid sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 128, 130, 144, 146, and 63-119,

(ii). nucleic acid sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 127, 129, 143, and 145.

According to PCT rule 13.2 and to the guidelines in Section (f)(i)(B)(1) of Annex B of the PCT administrative Instructions, all alternatives of a Markush Group must have a common structure. The amino acid/nucleic acid sequences are not regarded as being of similar nature because the nucleic acid/amino acid sequences

do not appear to share a common structure.

Applicant is advised that a reply to this requirement must include an identification of an amino acid/ nucleic acid sequence that is elected consonant with this requirement, and a listing of all claims readable thereon, including any claims subsequently added. An argument that a claim is allowable or that all claims are generic is considered nonresponsive unless accompanied by an election. The Examiner notes that this is not a species election requirement; rather it sets forth additional invention groups.

Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48 (b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a petition under 37 CFR 1.48 (b) and by the fee required under 37 CFR 1.17 (I).

Advisory Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ruixiang Li whose telephone number is (571) 272-0875. The examiner can normally be reached on Monday through Friday from 8:30 am to 5:00 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Nickol, can be reached on (571) 272-0835. The fax number for the organization where this application or proceeding is assigned is (571) 273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, please contact the Electronic Business Center (EBC) at the toll-free phone number 866-217-9197.

Ruixiang Li

Ruixiang Li, Ph.D.
Primary Examiner
May 11, 2007

RUIXIANG LI, PH.D.
PRIMARY EXAMINER

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 14, 2006, 01:34:23 ; Search time 75 Seconds
(without alignments)
3848.671 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MARAEGGASEQDDVSFLRTE.....RLADNAHDIWAKKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12295	78.1	5126	2	S40450	ryanodine receptor
2	6828	43.4	5107	2	T29144	partial CDS - Caen
3	6770.5	43.0	4969	2	A37113	ryanodine receptor
4	6769	43.0	4967	2	S72269	ryanodine receptor
5	6534.5	41.5	5037	1	AS4161	ryanodine-binding
6	6453.5	41.0	5035	1	I46646	ryanodine receptor
7	6442.5	40.9	5032	1	A35041	ryanodine receptor
8	6439	40.9	5037	2	B35041	ryanodine receptor
9	6438.5	40.9	4859	2	S74173	ryanodine receptor
10	6423	40.8	4869	2	S66572	ryanodine receptor
11	6419	40.8	4868	2	B54161	ryanodine-binding
12	6413	40.7	4872	2	S27272	ryanodine receptor
13	538	3.4	163	2	I47214	probable brain rya
14	520	3.3	162	2	I47213	cardiac muscle rya
15	327	2.1	2783	2	T31431	inositol 1,4,5-tri
16	323	2.1	2701	2	S17796	inositol-trisphosp
17	296.5	1.9	2693	2	A40743	IP3 receptor, XIP3
18	292.5	1.9	2695	2	BS4974	type 1 inositol 1,
19	290.5	1.8	2670	2	A46719	inositol 1,4,5-tri
20	289	1.8	2713	2	A55713	inositol 1,4,5-tri
21	286.5	1.8	2734	2	B36579	inositol 1,4,5-tri
22	285	1.8	2671	2	A49873	inositol 1,4,5-tri
23	284	1.8	1966	2	T32552	hypothetical prote
24	284	1.8	2848	2	T32550	hypothetical prote
25	279	1.8	2749	1	ACMSIT	inositol 1,4,5-tri
26	279	1.8	2749	2	A36579	inositol 1,4,5-tri
27	277.5	1.8	2833	2	A43360	inositol 1,4,5-tri
28	205	1.3	1676	2	B71410	probable centromer
29	203.5	1.3	2541	2	T29340	hypothetical prote
30	198	1.3	3259	1	A56539	giantin - human
31	198	1.3	5369	2	T44807	mycosubtilin synth
32	197.5	1.3	2954	2	T14156	kinesin-related pr
33	196.5	1.2	2218	2	B84683	hypothetical prote
34	192	1.2	1727	2	T50073	myosin-like coiled
35	192	1.2	3225	2	I52300	giantin - human
36	191	1.2	1882	2	T00069	hypothetical prote
37	189.5	1.2	2663	1	S28261	centromere protein
38	188.5	1.2	1642	2	T08880	NMDA receptor-bind
39	188	1.2	4540	2	T30838	cytoplasmic dynein
40	182.5	1.2	2331	2	T25410	hypothetical prote
41	182.5	1.2	3187	2	JC5837	364K Golgi complex
42	180.5	1.1	2712	2	T05113	hypothetical prote
43	179	1.1	6669	2	S55024	nebulin, skeletal
44	178	1.1	4151	2	T13734	groovin gene prote
45	177	1.1	52	2	I46644	ryanodine receptor

ALIGNMENTS

RESULT 1
S40450
ryanodine receptor/calcium release channel - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999
C;Accession: S40450
R;Takeshima, H.; Nishi, M.; Iwabe, N.; Miyata, T.; Hosoya, T.; Masai, I.; Hotta, Y.
FEBS Lett. 337, 81-87, 1994
A;Title: Isolation and characterization of a gene for a ryanodine receptor/calcium rel
A;Reference number: S40450; MUID:94102409; PMID:8276118
A;Accession: S40450
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5126 <TAK>
A;Cross-references: UNIPARC:UPI000017CF36
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homc

Query Match 78.1%; Score 12295; DB 2; Length 5126;
Best Local Similarity 77.5%; Pred. No. 0;
Matches 2348; Conservative 275; Mismatches 338; Indels 68; Gaps 22;

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Qy          1 MARAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
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Db          1 MARAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVPVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVPVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGRACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:|||||||:|||||||||:|||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNHLY 300
              |||||:|||| ||:|||||||||||| |||||||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNHLI 299

Qy        301 LVSREEATTASCAPCLRQKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |: | |||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFSW-QRKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDPSRSQEEESRTARVIRKCSSLPTKPINGL 420
              |||||||||||||||||||||||||||| ||||||||||:||||||||||||:|| |
Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDPSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFPASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
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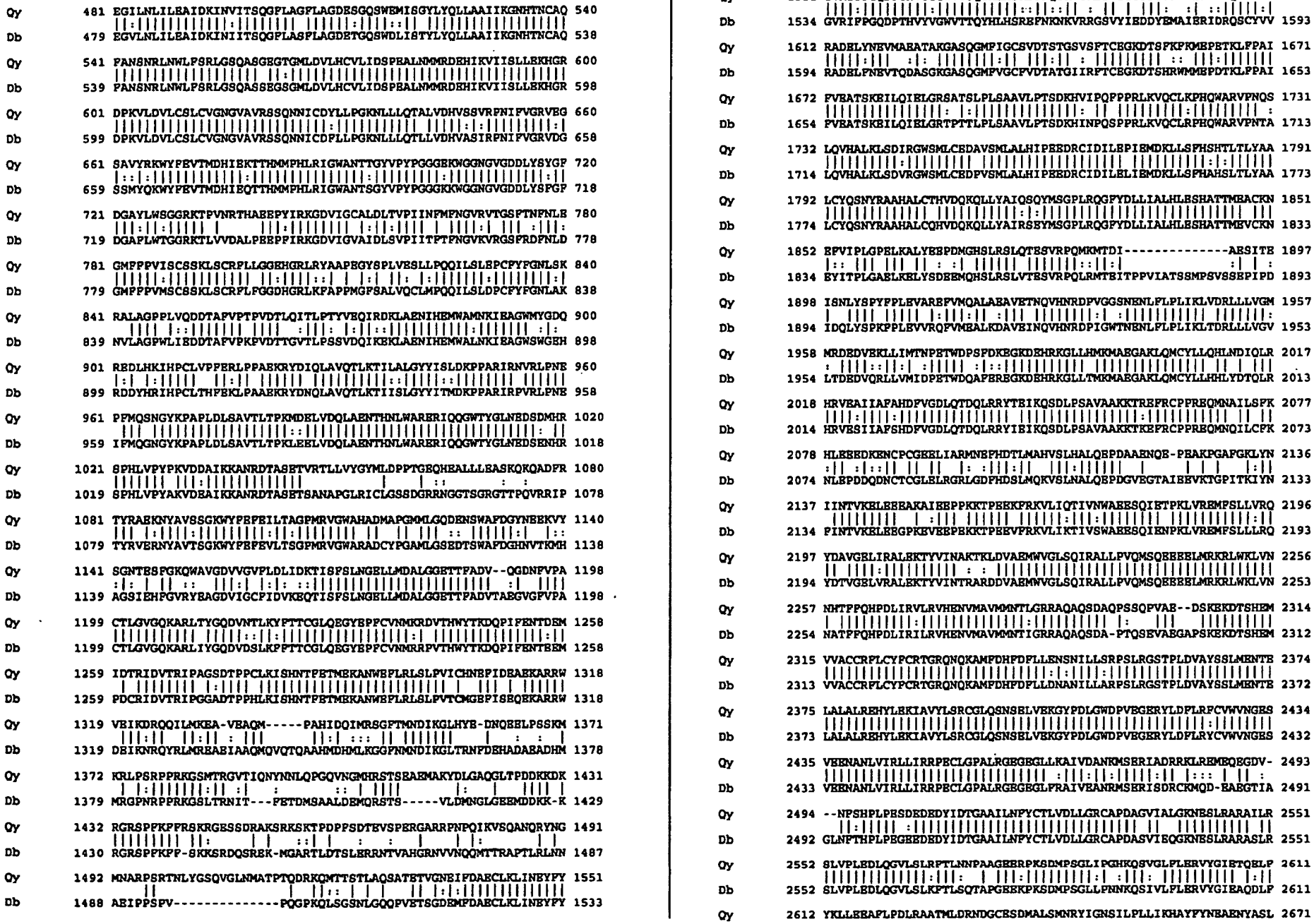
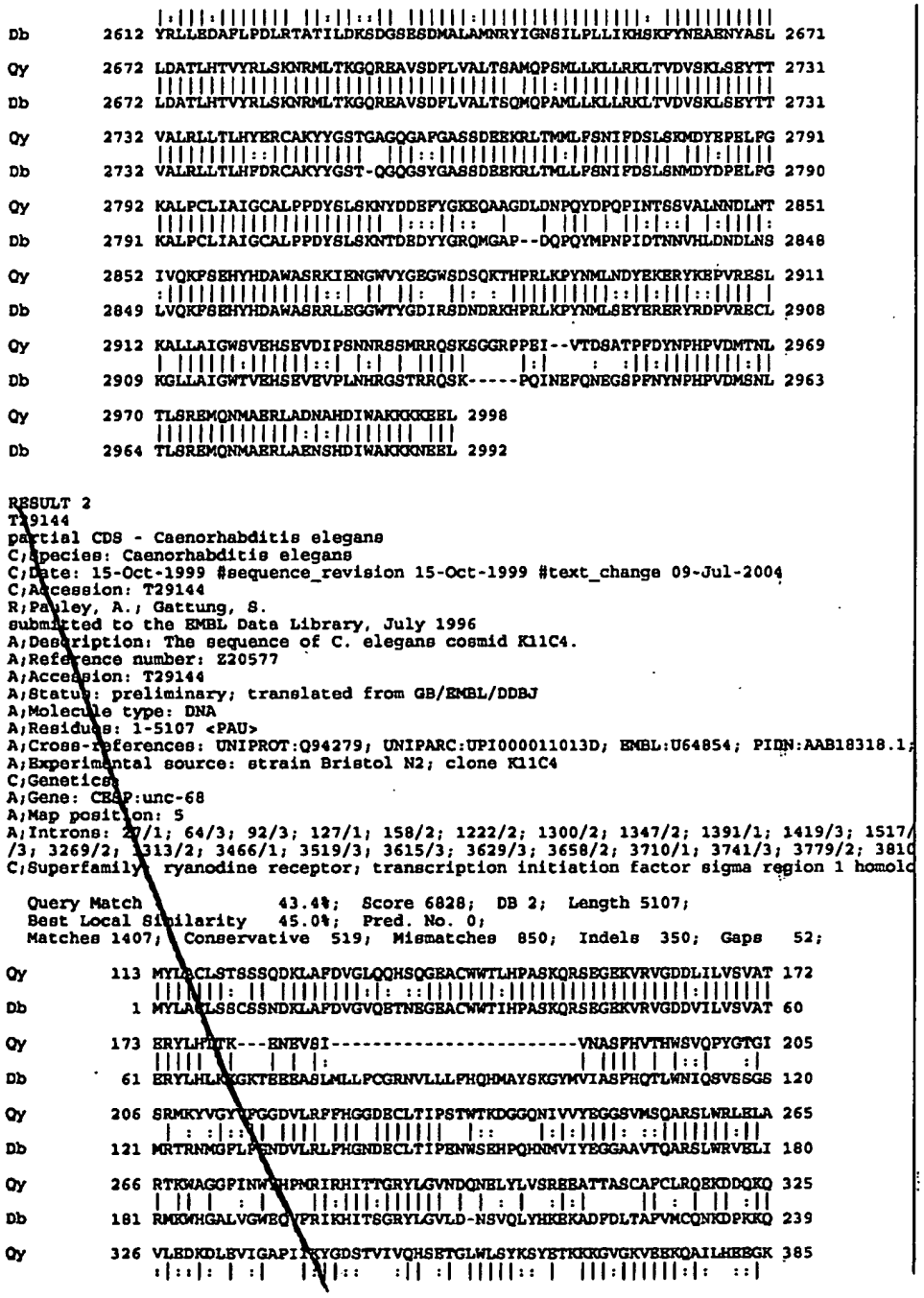
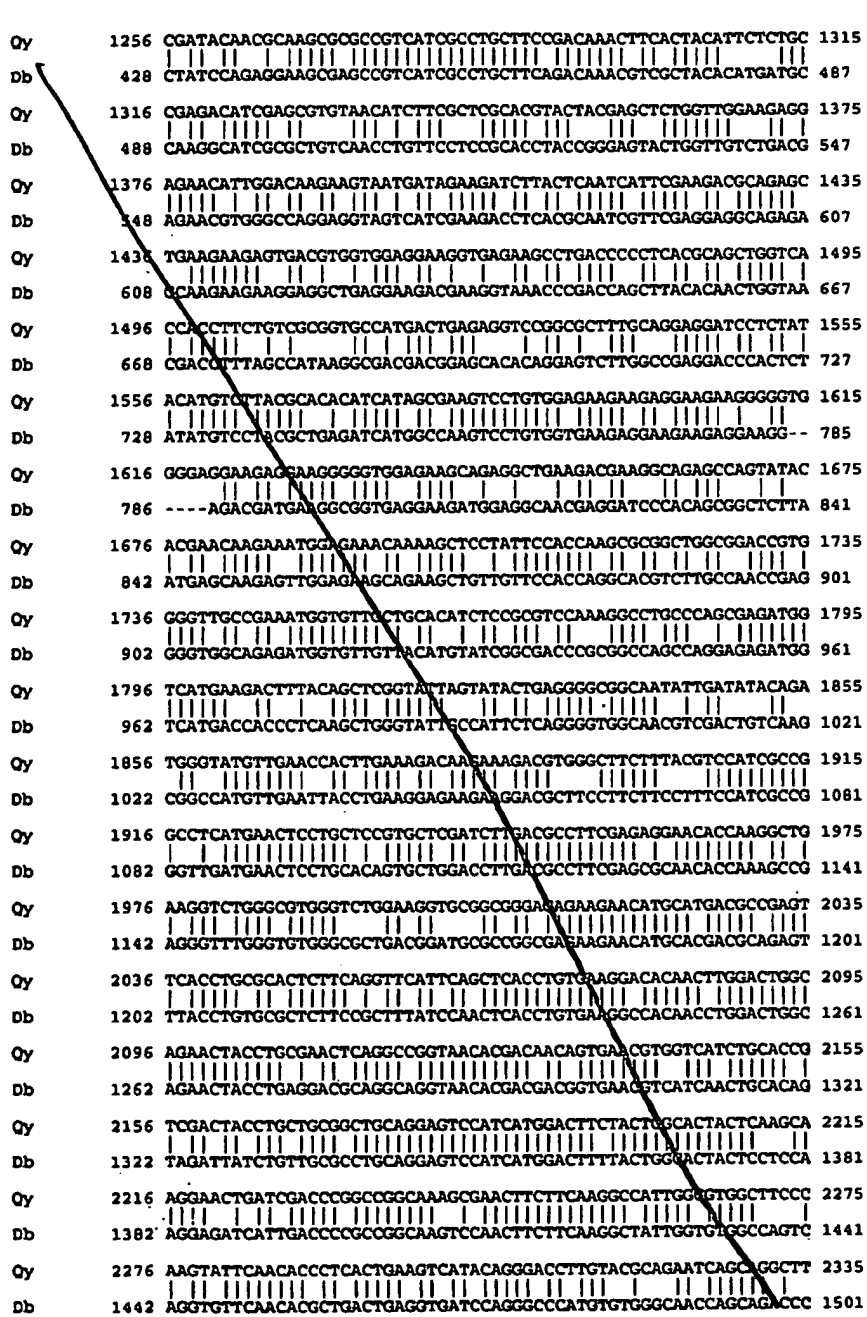
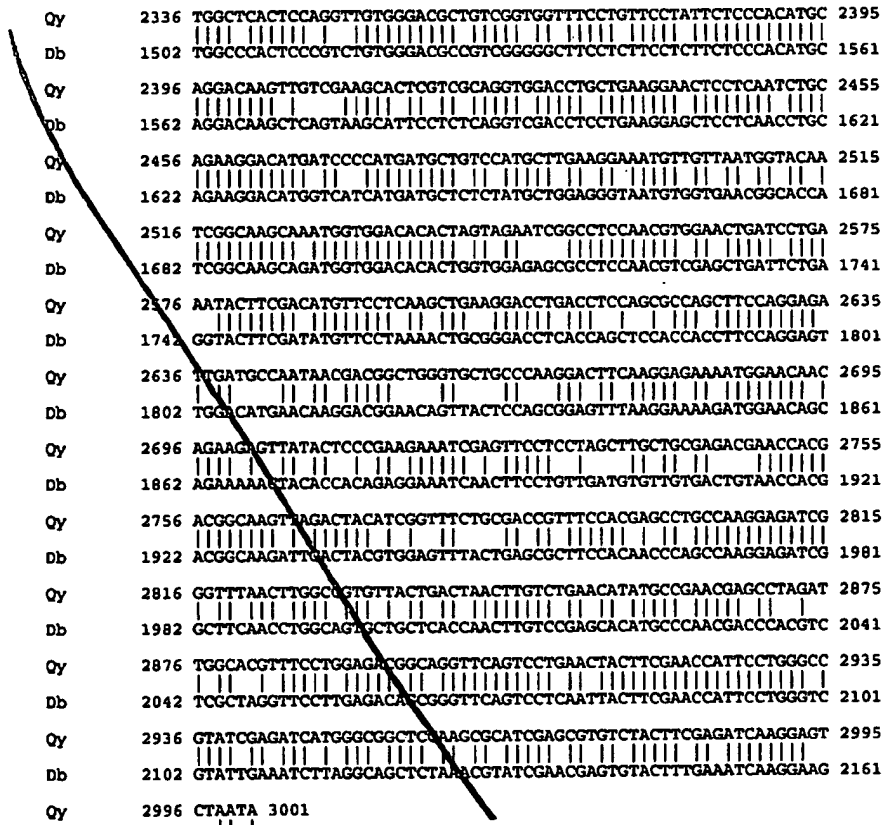




RESULT 2
T29144
partial CDS - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29144
R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid K11C4.
A;Reference number: Z20577
A;Accession: T29144
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5107 <PAU>
A;Cross-references: UNIPROT:Q94279; UNIPARC:UPI000011013D; EMBL:U64854; PIDN:AAB18318.1;
A;Experimental source: strain Bristol N2; clone K11C4
C;Genetics:
A;Gene: CESP:unc-68
A;Map position: 5
A;Introns: 27/1; 64/3; 92/3; 127/1; 158/2; 1222/2; 1300/2; 1347/2; 1391/1; 1419/3; 1517/
/3; 3269/2; 3313/2; 3466/1; 3519/3; 3615/3; 3629/3; 3658/2; 3710/1; 3741/3; 3779/2; 3810
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo

Query Match 43.4%; Score 6828; DB 2; Length 5107;
Best Local Similarity 45.0%; Pred. No. 0;
Matches 1407; Conservative 519; Mismatches 850; Indels 350; Gaps 52;





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RESULT 3
AF009344
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DEFINITION  Heliothis virescens ryanodine receptor (ryr) mRNA, partial cds.
ACCESSION   AF009344
VERSION     AF009344.1  GI:4102114
KEYWORDS    .
SOURCE      Heliothis virescens (tobacco budworm)
  ORGANISM  Heliothis virescens
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
            Noctuoidea; Noctuidae; Heliothinae; Heliothis.
REFERENCE   1  (bases 1 to 866)
  AUTHORS   Puente,E., Suner,M., Evans,A.D., McCaffery,A.R. and Windass,J.D.
  TITLE     Identification of a polymorphic ryanodine receptor gene from
            Heliothis virescens (Lepidoptera: noctuidae)
  JOURNAL   Insect Biochem. Mol. Biol. 30 (4), 335-347 (2000)
   PUBMED   10727900
REFERENCE   2  (bases 1 to 866)
  AUTHORS   Puente,E. and Windass,J.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1997) Biologie et Pathologie Digestive, INSERM
            U151, Institut Louis Bugnard. CHU Rangueil L3, Toulouse 31403 CEDEX
            04, France
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FEATURES             Location/Qualifiers
     source          1. .866
                     /organism="Heliothis virescens"
                     /mol_type="mRNA"
                     /strain="BRC"
                     /db_xref="taxon:7102"
                     /dev_stage="4th and 5th instar larvae"
     gene            <1. .>866
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                     /note="RyR; overlaps with AF009345"
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                     LWDAVGGPLFLFSHMQDKLSKHSSQVDLLKELLNLQKDMITMMLSMLEGNVVNGTIGK
                     QMVDTLVESASNVELILKYFDMFLKLKDLTSSASFQEIDANNDGWVLPKDFKEIMEQQ
                     KSYTPEEIEFLLA"
ORIGIN

  Query Match           27.8%;  Score 835.6;  DB 2;  Length 866;
  Best Local Similarity  97.8%;  Pred. No. 2e-173;
  Matches  847;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       1870 CACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTCATGAACTCC 1929
             ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db          1 CACTTGAAAGACAAGAAAGACGTGGGCTTCTTCACGTCCATCGCCGGCCTCATGAACTCC 60

Qy       1930 TGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGTCTGGGCGTG 1989
             ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCTCAGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGTCTGGGCGTG 120

Qy       1990 GGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACCTGCGCACTC 2049
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 GGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCAGAGTTCACCTGCGCACTC 180

Qy       2050 TTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAACTACCTGCGA 2109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAACTACCTGCGA 240

Qy       2110 ACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGACTACCTGCTG 2169
             |||||||||||||||||||||||||||||||||||||||||| || |||||||||||||||
Db        241 ACTCAGGCCGGTAACACGACGACAGTGAACGTGGTCATCTGTACTGTCGACTACCTGCTG 300

Qy       2170 CGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGAC 2229
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Qy       2230 CCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACC 2289
             |||||||||||||||| |||||||||||||||||| |||||||||||||||||||||||||
Db        361 CCGGCCGGCAAAGCGAATTTCTTCAAGGCCATTGGCGTAGCTTCCCAAGTATTCAACACC 420

Qy       2290 CTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGG 2349
             |||||||||||||||||||||||||||||||||||| ||||| || |||||||||||||||
Db        421 CTCACTGAAGTCATACAGGGACCTTGTACACAGAACCAACAGGCTTTGGCTCACTCCAGG 480

Qy       2350 TTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCG 2409
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTATGGGACGCTGTCGGTGGTTTCCTGTTCCTGTTCTCCCACATGCAGGACAAGTTGTCG 540

Qy       2410 AAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATC 2469
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2470 CCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATG 2529
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Qy       2530 GTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATG 2589
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Db        661 GTGGACACTCTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATG 720

Qy       2590 TTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGATGCCAATAAC 2649
             |||||||||||||||||||||||| |||||||| |||||||||||||||| ||||||||||
Db        721 TTCCTCAAGCTGAAGGACCTGACTTCCAGCGCTAGCTTCCAGGAGATAGATGCCAATAAC 780

Qy       2650 GACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAGAGTTATACT 2709
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Db        781 GACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAGAGTTATACT 840

Qy       2710 CCCGAAGAAATCGAGTTCCTCCTAGC 2735
             |||||||||||||||||||||||||||
Db        841 CCCGAAGAAATCGAGTTCCTCCTAGC 866


RESULT 4
OCRRR
LOCUS       OCRRR                   15361 bp    mRNA    linear   MAM 10-MAR-2001
DEFINITION  Rabbit skeletal muscle mRNA for ryanodine receptor.
ACCESSION   X15750
VERSION     X15750.1  GI:1709
KEYWORDS    calcium binding protein; channel protein; receptor; ryanodine
            receptor.
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
            Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 15361)
  AUTHORS   Takeshima,H., Nishimura,S., Matsumoto,T., Ishida,H., Kangawa,K.,
            Minamino,N., Matsuo,H., Ueda,M., Hanaoka,M., Hirose,T. and Numa,S.
  TITLE     Primary structure and expression from complementary DNA of skeletal
            muscle ryanodine receptor
  JOURNAL   Nature 339 (6224), 439-445 (1989)
   PUBMED   2725677
REFERENCE   2  (bases 1 to 15361)
  AUTHORS   Takeshima,H., Nishimura,S., Nishi,M., Ikeda,M. and Sugimoto,T.
  TITLE     A brain-specific transcript from the 3'-terminal region of the
            skeletal muscle ryanodine receptor gene
  JOURNAL   FEBS Lett. 322 (2), 105-110 (1993)
   PUBMED   8097730
REFERENCE   3  (bases 1 to 15361)
  AUTHORS   Numa,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-1989) Numa S., Kyoto University, Dept of Medical
            Chemistry and Molecular Genetics, Faculty of Medicine, Yoshida
            Sakyo-ku, Kyoto 606, Japan
COMMENT     *source: pRR72, pRR203, pRR308, pRR359, pRR451, pRR616. see X15749
            for ryanodine receptor gene 5' end; X15749 and X15750 seqs  are
            shown as a compiled one in [1]
            Data kindly reviewed (27-AUG-1989) by Numa S.
FEATURES             Location/Qualifiers
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                     /clone="pRR705, pRR256, pRR229,"
                     /tissue_type="skeletal muscle"
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     CDS             132. .15245
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                     /db_xref="UniProt/Swiss-Prot:P11716"
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                     RLCFLEPTSNAQNVPPDLAICCPFLEQSLSVRALQEMLANTVEAGVESSQGGGHRTLL
                     YGHAILLRHAHSRMYLSCLTTSRSVTDKLAFDVGLQEDATGEACWWTMHPASKQRSEG
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